

WO 00/24884

1

PCT/EP99/08323

SEQUENCE LISTING

5 <110> UNILEVER PLC
UNILEVER N.V

<120> ANTIGEN BINDING PROTEINS

10 <130> T3077

<140>
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15 <160> 45

<170> PatentIn Ver. 2.1

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25 <223> Description of Artificial Sequence:LINKER

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65 <400> 4

WO 0024884

2

PCT/EP99/08323

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- 5 <210> 5
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WO 00/24884

3

PCT/EP99/08323

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 Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala
 1 5 10 15
 ttc ctt ttc ctt ttg gct ggt ttt gca gcc aaa ata tct gcg cag gtg 95
 Phe Leu Phe Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val
 20 25 30
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35

40

<210> 14

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<212> PRT

<213> Artificial Sequence

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CONSTRUCT

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19

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25

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35

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

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Gly Thr Gln Val Thr Val Ser Ser

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<210> 16

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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

<400> 16

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<210> 17

<211> 188

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PLASMID
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WO 00/24884

5

PCT/EP99/08323

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    Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala
        1          5          10          15

    ttc ctt ttc ctt ttg gct ttt gca gcc aaa ata tct gcg cag gtg 95
15  Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val
        20          25          30

    cag ctg cag gag tca taatga ggg acc cag gtc acc gtc tcc tca gaa 143
20  Gln Leu Gln Gln Ser Gly Thr Gln Val Thr Val Ser Ser Glu
        35          40          45

    caa aaa ctc atc tca gaa gag gat ctg aat taatga ctt aag ctt 188
25  Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Xaa Lys Leu
        50          55

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35  Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala Phe
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    Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val Gln
        20          25          30

40  Leu Gln Glu Ser
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45  <210> 19
    <211> 19
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50  <223> Description of Artificial Sequence:PLASMID
        CONSTRUCT

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        1          5          10          15

55  Asp Leu Xaa

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60  <223> Description of Artificial Sequence:PLASMID
        CONSTRUCT

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WO 00/24884

6

PCT/EP99/08323

<400> 20
Xaa Lys Leu
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5

<210> 21
<211> 342
<212> DNA
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<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

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Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

25

tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt ggc ggc 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
20 25 30

30

ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg gtc 144
Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

35

gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg aag 192
Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
50 55 60

40

ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat ttg 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
65 70 75 80

45

gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt tac 288
Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

50

act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc gtc 336
Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
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tcc tca 342
Ser Ser

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<210> 22
<211> 114
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<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
20 25 30

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WO 00/24884

7

PCT/EP99/08323

Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
5 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
65 70 75 80

10 Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
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15 Ser Ser

20 <210> 23
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CONSTRUCT

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35 1 5 10 15

tct ctg aga ctc tcc tgt gca gcc tct gga cgc acc ggc agt acg tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
20 25 30

40 gac atg ggc tgg ttc cgc cag gct cca ggg aag gag cgt gag tct gta 144
Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
35 40 45

45 gca gct att aac tgg gat agt gcg cgc aca tac tat gca agc tcc gtg 192
Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
50 55 60

50 agg ggc cga ttc acc atc tcc aga gac aac gcc aag aag acg gtg tat 240
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
65 70 75 80

ctg caa atg aac agc ctg aaa cot gag cag acc gcc gtt tat acc tgt 288
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
55 85 90 95

ggc gcg ggg gaa ggt ggt act tgg gac tcc tgg ggc cag ggg acc cag 336
Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
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60 gtc acc gtc tcc tca 351
Val Thr Val Ser Ser
115

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WO 00/24884

8

PCT/EP99/08323

<210> 24
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 <212> PRT
 <213> Artificial Sequence
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 1 5 10 15
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 20 25 30
 15 Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
 35 40 45
 Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
 50 55 60
 20 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
 85 90 95
 25 Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
 100 105 110
 30 Val Thr Val Ser Ser
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<210> 25
 35 <211> 43
 <212> DNA
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 40 <223> Description of Artificial Sequence: PRIMER

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 gaattaagcg gccgcccagg tgaaactgct cgagtowggg gga 43

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<210> 26
 <211> 42
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 <213> Artificial Sequence

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<220>
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<210> 27
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<220>
 <223> Description of Artificial Sequence: PRIMER

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WO 00/24884

9

PCT/EP99/08323

<400> 27
caggtccagc tgcaggagtc tggg 24

5 <210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence:PRIMER

<400> 28
caggtgaac tgctcgagtc wggg 24

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<210> 29
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STRANDED

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Val Thr Val Ser Ser Gln Val Gln Leu Gln Glu Ser Xaa Xaa
1 5 10

40 aag ctt 55
Lys Leu
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45 <210> 30
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STRANDED

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55

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<211> 3
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STRANDED

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WO 00/24884

10

PCT/EP99/08323

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- 20 tcc tgt gca gcc tct gga cgc acc gcc agt acg tat gac atg gcc tgg 96
 Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp
 20 25 30
- 25 ttc cgc cag gct cca ggg aag gag cgt gag tct gta gca gct att aac 144
 Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn
 35 40 45
- 30 tgg gat agt gcg cgc aca tac tat gca agc tcc gtg agg gcc cga ttc 192
 Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe
 50 55 60
- 35 acc atc tcc aga gac aac gcc aag aag acg gtg tat ctg caa atg aac 240
 Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn
 65 70 75 80
- 40 agc ctg aaa cct gag gac acg gcc gtt tat acc tgt gcc gcg ggg gaa 288
 Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu
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- 45 ggt ggt act tgg gac tcc tgg gcc cag ggg acc cag gtc acc gtc tcc 336
 Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 100 105 110
- 50 tca cag gtg cag ctg cag gag tca ggg gga gcc ttg gtg cag gct ggg 384
 Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 115 120 125
- 55 gag tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt gcc 432
 Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly
 130 135 140
- 60 ggc ttc atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg 480
 Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Gly Lys Gln Arg Glu Leu
 145 150 155 160
- 65 gtc gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg 528
 Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val
 165 170 175
- aag ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat 576
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 180 185 190

11

PCT/EP99/08323

	ttg gaa atg aac agc ctg gaa cct gaa gac acg gct tat tac tgt	624
	Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys	
	195 200 205	
5	tac act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc	672
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	20 25 30	
25	Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn	
	35 40 45	
	Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe	
	50 55 60	
30	Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn	
	65 70 75 80	
	Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu	
	85 90 95	
35	Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser	
	100 105 110	
40	Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly	
	115 120 125	
	Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly	
	130 135 140	
45	Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu	
	145 150 155 160	
	Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val	
	165 170 175	
50	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr	
	180 185 190	
	Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys	
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55	Tyr Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr	
	210 215 220	
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WO 00/24884

12

PCT/EP99/08323

<220>
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15 <220>
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25 <210> 36
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 <212> DNA
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30 <220>
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35 <210> 37
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40 <220>
 <223> Description of Artificial Sequence:LINKER

45 <400> 37
 accatgaagg ccaagg 16

50 <210> 38
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50 <220>
 <223> Description of Artificial Sequence:LINKER

55 <400> 38
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60 <210> 39
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65 <220>
 <223> Description of Artificial Sequence:LINKER

WO 00/24884

13

PCT/EP99/08323

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10 <220>
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WO 00/24884

14

PCT/EP99/08323

<211> 25
<212> DNA
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